

OIPE

RAW SEQUENCE LISTING DATE: 05/16/2001
 PATENT APPLICATION: US/09/846,512 TIME: 13:26:22

Input Set : A:\10448-046002.TXT
 Output Set: N:\CRF3\05162001\I846512.raw

PS #2.

4 <110> APPLICANT: Meyers, Rachel A.
 5 MacBeth, Kyle J.
 7 <120> TITLE OF INVENTION: 14094, A NOVEL TRYPSIN FAMILY MEMBER AND
 8 USES THEREFOR
 10 <130> FILE REFERENCE: 10448-046002
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/846,512
 C--> 12 <141> CURRENT FILING DATE: 2001-05-01
 12 <150> PRIOR APPLICATION NUMBER: US 09/633,300
 13 <151> PRIOR FILING DATE: 2000-08-08
 15 <150> PRIOR APPLICATION NUMBER: US 60/200,621
 16 <151> PRIOR FILING DATE: 2000-04-28
 18 <160> NUMBER OF SEQ ID NOS: 13
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 2948
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (628)...(1986)
 31 <221> NAME/KEY: misc_feature
 32 <222> LOCATION: (1)...(2948)
 33 <223> OTHER INFORMATION: n = A,T,C or G
 35 <400> SEQUENCE: 1
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 37 gtttgtcaaa tccagttttc ttgtaaacat tggggggtaa ataacagagg tggcttatga 120
 38 gtattttcttc cagggtaaaa agcaaaagaa ttccggtttt ctgtatcctt ttcacttact 180
 39 gttaccctact ttgcctcgtc ttcacctgt ccaaacaccg gtctccaatt tgcccttcag 240
 40 agaacttaag tcaaggagag ttgaaattca caggccaggg cacatctttt atttatttca 300
 41 ttatgttggc caacagaact tgattgtaaa taataataaa gaaatctgtt atatactttc 360
 42 caaactccaa aaaaaaaccc gaattcagcc tggttaagtc caagctgaat tccgggtggg 420
 43 ggaaggaccg ggcaccggac ggctcgggta ctttcgttct taattaggtc atgcccgat 480
 44 gagccaggaa agggctgtgt ttatgggaag ccagtaacac tgtggcctac tatctcttcc 540
 45 gtggtgccat ctacattttt gggactcggg aattatgagg tagagggtga ggcggagccg 600
 46 gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt 654
 47 Met Gly Glu Asn Asp Pro Pro Ala Val
 48 1 5
 50 gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa 702
 51 Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys
 52 10 15 20 25
 54 ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 750
 55 Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu
 56 30 35 40
 58 tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att 798
 59 Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile
 60 45 50 55
 62 gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc 846

ENTERED

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63	Ala	Leu	Ile	Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	
64			60					65				70					
66	tca	ggg	aag	tac	aga	tgt	cgc	tca	tcc	ttt	aag	tgt	atc	gag	ctg	ata	894
67	Ser	Gly	Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	
68		75				80				85							
70	gct	cga	tgt	gac	gga	gtc	tcg	gat	tgc	aaa	gac	ggg	gag	gac	gag	tac	942
71	Ala	Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr	
72	90				95					100					105		
74	cgc	tgt	gtc	cgg	gtg	ggg	cag	aag	gcc	gtg	ctc	cag	gtg	ttc	aca		990
75	Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe	Thr	
76			110					115						120			
78	gct	gct	tcg	tgg	aag	acc	atg	tgc	tcc	gat	gac	tgg	aag	ggg	cac	tac	1038
79	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly	His	Tyr	
80			125					130					135				
82	gca	aag	gtt	gcc	tgt	gcc	caa	ctg	ggg	ttc	cca	agc	tat	gtg	agt	tca	1086
83	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr	Val	Ser	Ser	
84			140				145						150				
86	gat	aac	ctc	aga	gtg	agc	tcg	ctg	gag	ggg	cag	ttc	cgg	gag	gag	ttt	1134
87	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe	Arg	Glu	Glu	Phe	
88		155				160				165							
90	gtg	tcc	atc	gat	cac	ctc	ttg	cca	gat	gac	aag	gtg	act	gca	tta	cac	1182
91	Val	Ser	Ile	Asp	His	Leu	Pro	Asp	Asp	Lys	Val	Thr	Ala	Leu	His		
92	170				175					180				185			
94	cac	tca	gta	tat	gtg	agg	gag	gga	tgt	gcc	tct	ggc	cac	gtg	gtt	acc	1230
95	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala	Ser	Gly	His	Val	Val	Thr	
96			190					195					200				
98	ttg	cag	tgc	aca	gcc	tgt	ggg	cat	aga	agg	ggc	tac	agc	tca	cgc	atc	1278
99	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg	Arg	Gly	Tyr	Ser	Ser	Arg	Ile	
100			205					210					215				
102	gtg	ggg	gga	aac	atg	tcc	ttg	ctc	tcg	cag	tgg	ccc	tgg	cag	gcc	agc	1326
103	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu	Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	
104			220					225					230				
106	ctt	cag	ttc	cag	ggc	tac	cac	ctg	tgc	ggg	ggc	tct	gtc	atc	acg	ccc	1374
107	Leu	Gln	Phe	Gln	Gly	Tyr	His	Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	
108		235				240						245					
110	ctg	tgg	atc	atc	act	gct	gca	cac	tgt	gtt	tat	gac	ttg	tac	ctc	ccc	1422
111	Leu	Trp	Ile	Ile	Thr	Ala	Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	
112	250				255					260				265			
114	aag	tca	tgg	acc	atc	cag	gtg	ggg	cta	gtt	tcc	ctg	ttg	gac	aat	cca	1470
115	Lys	Ser	Trp	Thr	Ile	Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	
116			270							275				280			
118	gcc	cca	tcc	cac	ttg	gtg	gag	aag	att	gtc	tac	cac	agc	aag	tac	aag	1518
119	Ala	Pro	Ser	His	Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	
120			285					290					295				
122	cca	aag	agg	ctg	ggc	aat	gac	atc	gcc	ctt	atg	aag	ctg	gcc	ggg	cca	1566
123	Pro	Lys	Arg	Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	
124			300					305					310				
126	ctc	acg	ttc	aat	gaa	atg	atc	cag	cct	gtg	tgc	ctg	ccc	aac	tct	gaa	1614
127	Leu	Thr	Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	

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128      315      320      325
130 gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc      1662
131 Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
132 330      335      340      345
134 aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc      1710
135 Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val
136      350      355      360
138 cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc      1758
139 Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly
140      365      370      375
142 atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg      1806
143 Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val
144      380      385      390
146 gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg      1854
147 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg
148      395      400      405
150 agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca      1902
151 Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala
152 410      415      420      425
154 gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac      1950
155 Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp
156      430      435      440
158 tgg atc cac gag cag atg gag aga gac cta aaa acc tgaaaaggaa      1996
159 Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr
160      445      450
162 ggggacaagt agccacctga gttcctgagg tgatgaagac agcccgatcc tcccctggac      2056
163 tcccgtgtag gaacctgcac acgagcagac acccttggag ctctgagttc cggcaccagt      2116
164 agcaggcccg aaagaggcac ccttccatct gattccagca caaccttcaa gctgcttttt      2176
165 gttttttggt tttttgagat ggagtctcgc tctgttgccc aggctggagt gcagtggcga      2236
166 aatccctgct cactgcagcc tccgcttccc tggttcaagc gattctcttg cctcagcttc      2296
167 cccagtagct gggaccacag gtgcccgcga ccacacccaa ctaatttttg tatttttagt      2356
168 agagacaggg ttccaccatg ttggccaggc tgctctcaaa cccctgacct caaatgatgt      2416
169 gcctgcttca gcctcccaca gtgctgggat tacaggcatg ggccaccacg cctagcctca      2476
170 cgctcctttc tgatcttcac taagaacaaa agaagcagca acttgcaagg gcggcctttc      2536
171 ccaactggcc atctggtttt ctctccaggg gtcttgcaaa attcctgacg agataagcag      2596
172 ttatgtgacc tcacgtgcaa agccaccaac agccactcag aaaagacgca ccagcccaga      2656
173 agtgcagaac tgcagtcact gcacgttttc atctctaggg accagaacca aaccaccct      2716
174 ttctacttcc aagacttatt ttcacatgtg gggagggtta tctaggaatg actogtttaa      2776
175 ggocattttt catgatttct ttgtagcatt tgggtgctga cgtattattg tcccttgatt      2836
176 ccaaataata tgtttccctc cctcatwraa maaaaaaaaa aaaaaaaarr rmrrssgcta      2896
177 vavmarktta gagaaaaaac ctaccacrc cttccccctg aamctraaam ya      2948
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180 <211> LENGTH: 453
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 2
185 Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg
186 1 5 10 15
187 Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp

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188          20          25          30
189 Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
190          35          40          45
191 Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
192          50          55          60
193 Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
194 65          70          75          80
195 Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
196          85          90          95
197 Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
198          100         105         110
199 Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
200          115         120         125
201 Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
202          130         135         140
203 Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
204 145         150         155         160
205 Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
206          165         170         175
207 Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
208          180         185         190
209 Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
210          195         200         205
211 His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
212          210         215         220
213 Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
214 225         230         235         240
215 Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
216          245         250         255
217 His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
218          260         265         270
219 Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
220          275         280         285
221 Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
222          290         295         300
223 Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
224 305         310         315         320
225 Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
226          325         330         335
227 Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala
228          340         345         350
229 Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile
230          355         360         365
231 Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu
232          370         375         380
233 Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
234 385         390         395         400
235 Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly
236          405         410         415

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```

237 Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val
238           420           425           430
239 Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu
240           435           440           445
241 Arg Asp Leu Lys Thr
242           450
244 <210> SEQ ID NO: 3
245 <211> LENGTH: 1362
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 3
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251 cttgatgatt tgaaaataag tcctgttgca ccagatgcag atgctgttgc tgcacagatc      120
252 ctgtcactgc tgccattgaa gttttttcca atcatcgta ttgggatcat tgcattgata      180
253 ttagcactgg ccattggtct gggcatccac ttcgactgct cagggaaagta cagatgtcgc      240
254 tcatccttta agtgtatcga gctgatatgt cgatgtgacg gagtctcgga ttgcaaagac      300
255 ggggaggacg agtaccgctg tgtccgggtg ggtggtcaga atgccgtgct ccagggtgtt      360
256 acagctgctt cgtggaagac catgtgctcc gatgactgga agggtcacta cgcaaatgtt      420
257 gcctgtgccc aactgggttt cccaagctat gtgagttcag ataacctcag agtgagctcg      480
258 ctggaggggc agttccggga ggagtttgtg tccatcgata acctcttgcc agatgacaag      540
259 gtgactgcat tacaccactc agtatatgtg agggagggat gtgcctcttg ccacgtgggt      600
260 accttgcaat gcacagcctg tggatcataga aggggtacac gctcacgcac cgtgggtgga      660
261 aacatgtcct tgctctcgca gtggccctgg caggccagcc ttcagttcca gggctaccac      720
262 ctgtgcgggg gctctgtcat cacgccccctg tggatcatca ctgctgcaca ctgtgtttat      780
263 gacttgatcc tccccaaagc atggaccatc cagggtgggtc tagtttcctt gttggacaat      840
264 ccagcccatc cccacttggt ggagaagatt gtctaccaca gcaagtacaa gccaaagagg      900
265 ctgggcaatg acatcgccct tatgaagctg gccggggccac tcacgttcaa tgaaatgatc      960
266 cagcctgtgt gcctgcccaa ctctgaagag aacttccccg atggaaaagt gtgctggacg      1020
267 tcaggatggg gggccacaga ggatggaggt gacgcctccc ctgtcctgaa ccacgcggcc      1080
268 gtccctttga tttccaacaa gatctgcaac cacagggacg tgtacgggtg catcatctcc      1140
269 cctccatgc tctgcgcggg ctacctgacg ggtggcgttg acagctgcca gggggacagc      1200
270 ggggggcccc tgggtgtgta agagaggagg ctgtggaagt tagtgggagc gaccagcttt      1260
271 ggcacgagct gcgcagaggt gaacaagcct ggggtgtaca cccgtgtcac ctccttcctg      1320
272 gactggatcc acgagcagat ggagagagac ctaaaaacct ga      1362
274 <210> SEQ ID NO: 4
275 <211> LENGTH: 260
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
280 <223> OTHER INFORMATION: consensus sequence
282 <400> SEQUENCE: 4
283 Ile Val Gly Gly Arg Glu Ala Gln Pro Gly Ser Phe Gly Ser Pro Trp
284 1           5           10           15
285 Gln Val Ser Leu Gln Val Arg Ser Gly Gly Gly Ser Arg Lys His Phe
286           20           25           30
287 Cys Gly Gly Ser Leu Ile Ser Glu Asn Trp Val Leu Thr Ala Ala His
288           35           40           45
289 Cys Val Ser Gly Ala Ala Ser Ala Pro Ala Ser Ser Val Arg Val Ser
290           50           55           60

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11